

```

      11      20      29      38      47      56
5' ACG NGA ATG GCC TTC CCG CGC CCC AAG AAG AAC CTG CCC CAG CCC AAG NAG GCT
      M  A  F  P  R  P  K  K  N  L  P  Q  P  K  X  A

      65      74      83      92      101      110
GCC ACA GAG GGC CCC AGT GCT GCC TCT GGT GTG CCC CAG ACG GGA CCT GGC AGG
A  T  E  G  P  S  A  A  S  G  V  P  Q  T  G  P  G  R

      119      128      137      146      155      164
GAG GTG GCA GCC ACC CGG CCC AAG ACC ACC AAG TCG GGG AAG GCG CTG GCC AAG
E  V  A  A  T  R  P  K  T  T  K  S  G  K  A  L  A  K

      173      182      191      200      209      218
ACT CGG TGG GTG GAG CCT CAG AAT GTT GTG GCA GCA GCT GCT GCC AAG GCC AAG
T  R  W  V  E  P  Q  N  V  V  A  A  A  A  A  K  A  K

      227      236      245      254      263      272
ATG GCC ACG AGC ATC CCT GAG CCG GAG GGT GCA GCT GCT GCC ACT GCT CAG CAC
M  A  T  S  I  P  E  P  E  G  A  A  A  A  T  A  Q  H

      281      290      299      308      317      326
AGT GCT GAG CCC TGG GCC AGG ATG GGA GGC AAG AGG ACC AAG AAG TCC AAG CAC
S  A  E  P  W  A  R  M  G  G  K  R  T  K  K  S  K  H

      335      344      353      362      371      380
CTG GAT GAT GAG TAT GAG AGC AGC GAG GAG GAG AGA GAG ACT CCC GCG GTC CCA
L  D  D  E  Y  E  S  S  E  E  E  R  E  T  P  A  V  P

      389      398      407      416      425      434
CCC ACC TGG AGA GCA TCA CAG CCC TCA TTG ACG GTG CGG GCT CAG TTG GCC CCT
P  T  W  R  A  S  Q  P  S  L  T  V  R  A  Q  L  A  P

      443      452      461      470      479      488
CGG CCC CCG ATG GCC CCG AGG TCC CAG ATA CCC TCA AGG CAC GTA CTG TGC CTG
R  P  P  M  A  P  R  S  Q  I  P  S  R  H  V  L  C  L

      497      506      515      524      533      542
CCC CCC CGC AAC GTG ACC CTT CTG CAG GAG AGG GCA AAT AAG TTG GTG AAA TAC
P  P  R  N  V  T  L  L  Q  E  R  A  N  K  L  V  K  Y

      551      560      569      578      587      596
CTG ATG ATT AAG GAC TAC AAG AAG ATC CCC ATC AAG CGC GCA GAC ATG CTG AAG
L  M  I  K  D  Y  K  K  I  P  I  K  R  A  D  M  L  K

```

FIGURE 1A

GAT	GTC	ATC	AGA	GAA	TAT	GAT	GAA	CAT	TTC	CCT	GAG	ATC	ATT	GAA	CGA	GCA	ACG
D	V	I	R	E	Y	D	E	H	F	P	E	I	I	E	R	A	T
TAC	ACC	CTG	GAA	AAG	TTT	GGG	ATC	CAC	CTG	AAG	GAG	ATC	GAC	AAG	GAA	GAA	
Y	T	L	E	K	K	F	G	I	H	L	K	E	I	D	K	E	E
CAC	CTG	TAT	ATT	CTT	GTC	TGC	ACA	CGG	GAC	TCC	TCA	GCT	CGC	CTC	CTT	GGA	AAA
H	L	Y	I	L	V	C	T	R	D	S	S	A	R	L	L	G	K
ACC	AAG	GAC	ACT	CCC	AGG	CTG	AGT	CTC	CTC	TTG	GTG	ATT	CTG	GGC	GTC	ATC	TTC
T	K	D	T	P	R	L	S	L	L	L	V	I	L	G	V	I	F
ATG	AAT	GGC	AAC	CGT	GCC	AGC	GAG	GCT	GTC	CTC	TGG	GAG	GCA	CTA	CGC	AAG	ATG
M	N	G	N	R	A	S	E	A	V	L	W	E	A	L	R	K	M
GGA	CTG	CGT	CCT	GGG	GTG	AGA	CAT	CCC	CTC	CTT	GGA	GAT	CTA	AGG	AAA	CTT	CTC
G	L	R	P	G	V	R	H	P	L	L	G	D	L	R	K	L	L
ACC	TAT	GAG	TTT	GTA	AAG	CAG	AAA	TAC	CTG	GAC	TAC	AGA	CGA	GTG	CCC	AAC	AGC
T	Y	E	F	V	K	Q	K	Y	L	D	Y	R	R	V	P	N	S
AAC	CCC	CCG	GAG	TAT	GAG	TTC	CTC	TGG	GGC	CTC	CGT	TCC	TAC	CAT	GAG	ACT	AGC
N	P	P	E	Y	E	F	L	W	G	L	R	S	Y	H	E	T	S
AAG	ATG	AAA	GTG	CTG	AGA	TTC	ATT	GCA	GAG	GTT	CAG	AAA	AGA	GAC	CCT	CGT	GAC
K	M	K	V	L	R	F	I	A	E	V	Q	K	R	D	P	R	D
TGG	ACT	GCA	CAG	TTC	ATG	GAG	GCT	GCA	GAT	GAG	GCC	TTG	GAT	GCT	CTG	GAT	GCT
W	T	A	Q	F	M	E	A	A	D	E	A	L	D	A	L	D	A
GCT	GCA	GCT	GAG	GCC	GAA	GCC	CGG	GCT	GAA	GCA	AGA	ACC	CGC	ATG	GGA	ATT	GGA
A	A	A	E	A	E	A	R	A	E	A	R	T	R	M	G	I	G
GAT	GAG	GCT	GTG	TCT	GGG	CCC	GGA	GCT	GGG	ATG	ACA	TTG	AGT	TTG	AGC	TGC	TGA
D	E	A	V	S	G	P	G	A	G	M	T	L	S	L	S	C	

CCT 3'

FIGURE 1B

FIGURE 2A

268	F	M	N	G	N	R	A	S	E	A	V	L	W	E	A	L	R	K	M	G	L	R	P	G	V	R	H	P	L	L	SEQ ID NO-1		
209	F	L	K	G	N	S	A	T	E	E	E	I	W	K	F	M	N	V	L	G	A	Y	D	G	E	E	H	L	I	Y	GI 608993		
235	F	I	E	G	Y	C	T	P	E	E	V	I	W	E	A	L	N	M	M	G	L	Y	D	G	M	E	H	L	I	Y	GI 533511		
253	F	M	K	G	N	R	A	T	E	Q	E	V	W	Q	F	L	H	G	V	G	V	Y	A	G	K	K	H	L	I	F	GI 1165170		
203	Y	V	K	G	R	G	A	R	E	G	A	V	W	N	V	L	R	I	L	G	L	R	P	W	K	K	H	S	T	F	GI 1040691		
298	G	D	L	R	K	L	L	T	Y	E	F	V	K	Q	K	Y	L	D	Y	R	R	V	P	N	S	N	P	P	E	Y	SEQ ID NO-1		
239	G	E	P	R	K	F	I	T	Q	D	L	V	Q	E	K	Y	L	K	Y	E	Q	V	P	N	S	D	P	P	R	Y	GI 608993		
265	G	E	P	R	K	L	L	T	Q	D	W	V	Q	E	N	Y	L	E	Y	R	Q	V	P	G	S	D	P	A	R	Y	GI 533511		
283	G	E	P	E	E	F	I	-	R	D	V	V	R	E	N	Y	L	E	Y	R	Q	V	P	G	S	D	P	P	S	Y	GI 1165170		
233	G	D	V	R	K	I	I	T	E	E	F	V	Q	Q	N	Y	L	K	Y	Q	R	V	P	H	I	E	P	P	E	Y	GI 1040691		
328	E	F	L	W	G	L	R	S	Y	H	E	T	S	K	M	K	V	L	R	F	I	A	E	V	Q	K	R	D	P	R	SEQ ID NO-1		
269	Q	F	L	W	G	P	R	A	Y	A	E	T	T	K	M	K	V	L	E	F	L	A	K	M	N	G	A	T	P	R	GI 608993		
295	E	F	L	W	G	P	R	A	H	A	E	I	R	K	M	S	L	L	K	F	L	A	K	V	N	G	S	D	P	R	GI 533511		
312	E	F	L	W	G	P	R	A	H	A	E	T	T	K	M	K	V	L	E	V	L	A	K	V	N	G	T	V	P	S	GI 1165170		
263	E	E	F	W	G	S	R	A	N	R	E	I	T	K	M	Q	I	M	E	F	L	A	R	V	F	K	K	D	P	Q	GI 1040691		
358	D	W	T	A	Q	F	M	E	A	A	D	E	A	L	D	A	L	D	A	A	A	A	E	A	E	A	R	A	E	A	SEQ ID NO-1		
299	D	F	P	S	H	Y	E	E	-	-	-	-	-	-	-	-	A	L	R	D	E	E	E	R	A	Q	V	R	S	S	V	GI 608993	
325	S	F	P	L	W	Y	E	E	-	-	-	-	-	-	-	-	A	L	K	D	E	E	E	R	A	Q	D	R	I	A	T	GI 533511	
342	A	F	P	N	L	Y	Q	L	-	-	-	-	-	-	-	-	A	L	R	D	Q	A	-	-	-	-	-	-	-	G	G	GI 1165170	
293	A	W	P	S	R	Y	R	E	A	L	E	Q	A	-	R	A	L	R	E	A	N	L	A	A	O	A	P	-	-	-	-	GI 1040691	
388	R	T	R	M	G	I	G	D	E	A	V	S	G	P	G	A	G	M	T	L	S	L	S	C								SEQ ID NO-1	
322	R	A	R	R	R	T	T	A	T	T	F	R	A	R	S	R	A	-	P	F	S	R	S	S	H	P	M						GI 608993
348	T	D	D	T	T	A	M	A	S	A	-	S	S	S	A	T	G	-	S	F	S	-	-	-	Y	P	E						GI 533511
358	V	P	R	R	R	V	Q	G	K	G	V	H	S	K	A	P	-	-	-	-	S	Q	K	S	S	N	M						GI 1165170
319	-	-	R	S	S	V	S	E	D																						GI 1040691		

FIGURE 2B

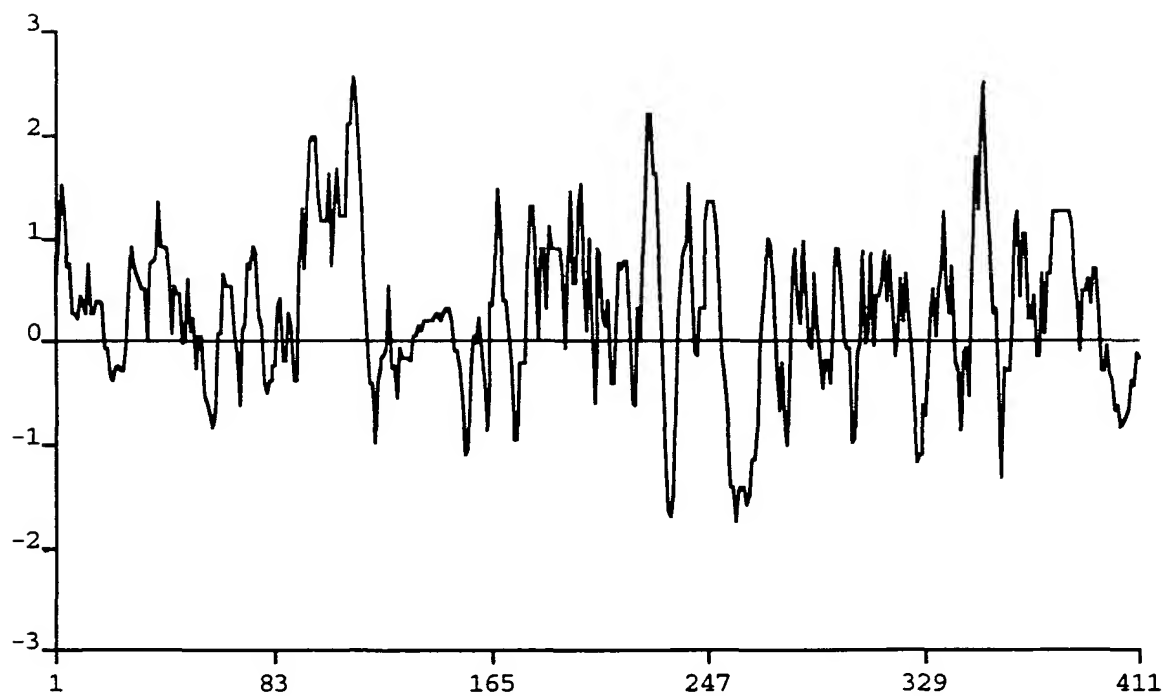


FIGURE 3

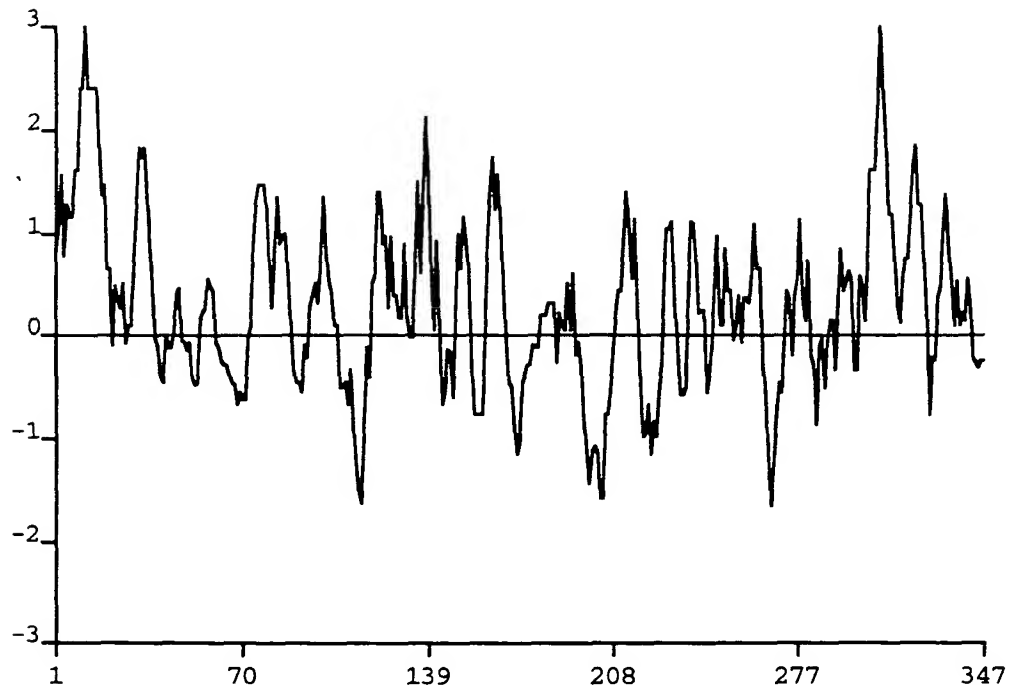


FIGURE 4